SEQUENCE LISTING

<110> Yeh, Chau-Ting

<120> NOVEL VIRAL SEQUENCES

<130> 14176-003001

<140> US 10/730,632
<141> 2003-12-08

<150> US 60/440,948
<151> 2003-01-17

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 364
<212> DNA
<213> Unknown

<220>
<221> CDS
<222> (1)...(364)

<223> Viral sequence NV-F

<400> 1

```
gac tgt tgg tgg cac aaa gcc ccg agc aaa gtt ggc aac ccc cgc cgt       48
Asp Cys Trp Trp His Lys Ala Pro Ser Lys Val Gly Asn Pro Arg Arg
 1               5                  10                  15

cac tca gcc ctg caa gaa gcc act tgc gtc ctc cac aac tcc cca aag       96
His Ser Ala Leu Gln Glu Ala Thr Cys Val Leu His Asn Ser Pro Lys
            20                  25                  30

ttg tta ctg gtg tac caa tcg gag gca gcc gag ggg atg tat aaa gaa      144
Leu Leu Leu Val Tyr Gln Ser Glu Ala Ala Glu Gly Met Tyr Lys Glu
        35                  40                  45

ata gca aag gaa ttc gcg aaa ggg aaa gga aag aag gag agg aaa cta      192
Ile Ala Lys Glu Phe Ala Lys Gly Lys Gly Lys Lys Glu Arg Lys Leu
    50                  55                  60

aag aag aaa aaa atg ctt tcg ggt att acg gaa gaa ggt tct cca cag      240
Lys Lys Lys Lys Met Leu Ser Gly Ile Thr Glu Glu Gly Ser Pro Gln
65                  70                  75                  80

cag tcc tct tct gct ccg ggc ctg gag gga gag agc gag acc aca aag      288
Gln Ser Ser Ser Ala Pro Gly Leu Glu Gly Glu Ser Glu Thr Thr Lys
                85                  90                  95

atg atg agc aaa aaa ttc caa gac atg acg aat ccg caa aag aag aaa      336
```

Met Met Ser Lys Lys Phe Gln Asp Met Thr Asn Pro Gln Lys Lys Lys
100 105 110

aag aaa cgg acc agt ctg ctc ctt aac t 364
Lys Lys Arg Thr Ser Leu Leu Leu Asn
115 120

<210> 2
<211> 121
<212> PRT
<213> Unknown

<220>
<223> Viral sequence NV-F

<400> 2
Asp Cys Trp Trp His Lys Ala Pro Ser Lys Val Gly Asn Pro Arg Arg
1 5 10 15
His Ser Ala Leu Gln Glu Ala Thr Cys Val Leu His Asn Ser Pro Lys
20 25 30
Leu Leu Leu Val Tyr Gln Ser Glu Ala Ala Glu Gly Met Tyr Lys Glu
35 40 45
Ile Ala Lys Glu Phe Ala Lys Gly Lys Gly Lys Lys Glu Arg Lys Leu
50 55 60
Lys Lys Lys Lys Met Leu Ser Gly Ile Thr Glu Glu Gly Ser Pro Gln
65 70 75 80
Gln Ser Ser Ser Ala Pro Gly Leu Glu Gly Glu Ser Glu Thr Thr Lys
85 90 95
Met Met Ser Lys Lys Phe Gln Asp Met Thr Asn Pro Gln Lys Lys Lys
100 105 110
Lys Lys Arg Thr Ser Leu Leu Leu Asn
115 120

<210> 3
<211> 20
<212> DNA
<213> Unknown

<220>
<223> Primer

<400> 3
tgttggtggc acaaagcccc 20

<210> 4
<211> 20
<212> DNA
<213> Unknown

<220>
<223> Primer

<400> 4
ctttgtggtc tcgctctctc 20

<210> 5

<211> 20
<212> DNA
<213> Unknown

<220>
<223> Primer

<400> 5
gcaaagttgg caacccccgc 20

<210> 6
<211> 20
<212> DNA
<213> Unknown

<220>
<223> Primer

<400> 6
ctccaggccc ggagcagaag 20

<210> 7
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> 7-10
<223> n = mixture of A, T, C, and G in equal ratios

<400> 7
ccgcggnnnn 10

<210> 8
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> 7-10
<223> n = mixture of A, T, C, and G in equal ratios.

<400> 8
gaattcnnnn 10

<210> 9
<211> 34
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 9
gcttgctctg tctctttttt ttttttttttt tttt 34